

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Hadlaczky, Gyula  
Szalay, Aladar
- (ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Heller Ehrman White & McAuliffe
  - (B) STREET: 4250 Executive Square, 7th Floor
  - (C) CITY: La Jolla
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 28-NOV-2000
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/835,431
  - (B) FILING DATE: 10-APR-1997
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/695,191
  - (B) FILING DATE: 07-AUG-1996
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/682,080
  - (B) FILING DATE: 15-JUL-1996
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/629,822
  - (B) FILING DATE: 10-APR-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Seidman, Stephanie L
  - (B) REGISTRATION NUMBER: 33,779
  - (C) REFERENCE/DOCKET NUMBER: 24601-402F
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 858-450-8403
  - (B) TELEFAX: 858-587-5360
  - (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:  
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTNCCATGA	TTTAAAGTTT	60
TCTCGCCATA	TTCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTNCACGTT	TTNCAGTGAT	120
TTCGTCAATT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTT	AGTTTTCTCT	240
GCCATATTTT	ACGTCCTAAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTTCCAG	GTCCTATAAT	GTGCATTTCT	CATTTNNCAC	GTTTTTCAGT	GATTTCTGTC	360
TTTTTTCAAG	TCGGCAAGTG	GATGTTTCTC	ATTNNCCATG	ATTNNCAGTT	TTCTTGNAAT	420
ATTCCATGTC	CTACAATGAT	CATTTTTTAAT	TTTCCACCTT	TTCATTTTTT	CACGCCATAT	480
TTCATGTCCT	AAAGTGTATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTTTCT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTTT	CACCTTTTTT	ACTGATTTTC	TCATTTTTTCA	600
AGTCGTCAAC	TGGATCTTTC	TAATTTTCCA	TGATTTTCAG	TTATCTTGTC	ATATTCCATG	660
TCCTACAGTG	GACATTTCTA	AATTTTCCAA	CTTTTCAAT	TTTTCTCGAC	ATATTTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTCACGT	TTTTTCAGTG	TTTCGTCATT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTTT	CTTGCTATAT	TCCATGTCCT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTTC	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCCTT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTT	ACGTTTTTCA	GTAATTTCTT	CATTTTTTAA	GCCCTCAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTACAG	TCCTAAAGTG	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTTTCACGT	TTTCAGTGAA	TTC			1293

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1044 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:  
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAAACT	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTTGAA	GCTTTCTTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAAC	GGGATTGTCT	TATATAAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
AACTCTTTT	TTGTAGTATC	TGGAAGTGGA	CATTTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTGT	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTTGTCT	AGCTTTGAGG	ATTTCTGTTG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTCCC	AGAAACTTCT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660

GGATGTGGAC	ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCTCGAA	720
AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTG	CGCCCTCAAC	TAACAGTGT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTTGA	AACACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAAG	CAGACAGCAG	900
CATTTCCAGA	ATCTTGTGTT	TGATGTTTGC	ATTCAAATCA	CAGAGTTGAA	CATTTCCCTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
AATGGGACAG	GC'TTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGGTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCTCTG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGCG	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCTTG	TTTTTCCTTC	AGCAATTTTG	CATTTTAA	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTTGT	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTTCTTGN	NTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTATTTG	CAAATATTTT	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCAC TTC	1260
TTTTGTGTAT	ATCTACCTTT	TGTGTCATTT	GTTAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAAG	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCTCCTGG	AAAAGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACTTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATTC	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAA	GCATCGCTCA	GTCCCACCTC	TCCCTATTTT	TCTACAATAA	ACTCTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280

TTGAATTTAC AGAAGTGATG GGCTTAATAA CTGGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340  
 CCGTCACACC GGGAGCAAGA GTGCGCTGCE TAGTCGCCAT CTGCCCCGAG GTGGCGGCTG 2400  
 CCTCGACACT GACAGCAATA GGGTCCGSCA GTCTCCGAG CTGCCAGCAG GGGCGGTACG 2460  
 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCA GTTGA 28

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic LNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: RNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT  
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT  
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC	TTA	AAG	ATG	ACT	TCG	AAA	GTT	TAT	GAT	CCA	GAA	CAA	AGG	AAA	CGG	48
Ser	Leu	Lys	Met	Thr	Ser	Lys	Val	Tyr	Asp	Pro	Glu	Gln	Arg	Lys	Arg	
1				5					10					15		
ATG	ATA	ACT	GGT	CCG	CAG	TGG	TGG	GCC	AGA	TGT	AAA	CAA	ATG	AAT	GTT	96
Met	Ile	Thr	Gly	Pro	Gln	Trp	Trp	Ala	Arg	Cys	Lys	Gln	Met	Asn	Val	
			20					25					30			
CTT	GAT	TCA	TTT	ATT	AAT	TAT	TAT	GAT	TCA	GAA	AAA	CAT	GCA	GAA	AAT	144
Leu	Asp	Ser	Phe	Ile	Asn	Tyr	Tyr	Asp	Ser	Glu	Lys	His	Ala	Glu	Asn	
		35				40						45				
GCT	GTT	ATT	TTT	TTA	CAT	GGT	AAC	GCG	GCC	TCT	TCT	TAT	TTA	TGG	CGA	192
Ala	Val	Ile	Phe	Leu	His	Gly	Asn	Ala	Ala	Ser	Ser	Tyr	Leu	Trp	Arg	
	50					55				60						
CAT	GTT	GTG	CCA	CAT	ATT	GAG	CCA	GTA	GCG	CGG	TGT	ATT	ATA	CCA	GAT	240
His	Val	Val	Pro	His	Ile	Glu	Pro	Val	Ala	Arg	Cys	Ile	Ile	Pro	Asp	
65					70				75						80	
CTT	ATT	GGT	ATG	GGC	AAA	TCA	GGC	AAA	TCT	GGT	AAT	GGT	TCT	TAT	AGG	288
Leu	Ile	Gly	Met	Gly	Lys	Ser	Gly	Lys	Ser	Gly	Asn	Gly	Ser	Tyr	Arg	
				85				90					95			
TTA	CTT	GAT	CAT	TAC	AAA	TAT	CTT	ACT	GCA	TGG	TTG	AAC	TTC	TTA	ATT	336
Leu	Leu	Asp	His	Tyr	Lys	Tyr	Leu	Thr	Ala	Trp	Leu	Asn	Phe	Leu	Ile	
			100					105					110			
TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
		115					120					125				
GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
	130					135					140					
CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
145					150				155						160	
GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
				165				170					175			
ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
			180					185					190			
ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624

Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro	
195 200 205	
TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT	672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg	
210 215 220	
GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT	720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val	
225 230 235 240	
AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG	768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met	
245 250 255	
TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC	816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly	
260 265 270	
GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT	864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His	
275 280 285	
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG	912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser	
290 295 300	
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA	945
Phe Val Glu Arg Val Leu Lys Asn Glu Gln	
305 310	

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTGTGTCAC

30

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAAGTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	GACTGACACC	ATTAACACTT	TGTCAGCCTC	AGTGACTACA	GTCATAGATG	240
AACAGGCCTC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTCCA	GATACAACCTA	GATGTATTAT	GACAAATAAC	TCAGCAGGGA	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATTC	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAAG	TCTTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGAATTT	GAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGGA	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAATTG	GATCTCCTCA	GCATTTTCTT	TCTTTAAAAA	ATGGGTGGGA	TTAATATTAT	600
TTGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGGTCTGT	AAGCTTAAGG	660
CCCAAAGTAG	GAGAGACAAG	GTGGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGAG	TGTGCTTCAG	CAGCCCGAGA	840
GAGTTGCAAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTTCAT	GAAGGTTTCT	TGTCCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTCAGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCCTG	1020
TACATGGCTC	CTTTACCTAC	ACACTGGGGA	TTTGACCTCT	ATCTCCACTC	TCATTAATAT	1080
GGGTGGCCTA	TTTGCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GTTGGGAGCC	GCGCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTTCTAAGTG	GTAACAAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GTGGTTCTTC	ACTCCATGTG	CTCTGCCTTC	CCCGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCCTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTCT	CTCTCTCTCT	TGCTTCTCTC	TCTTGCTTTT	TCGCTCTCTT	1380
GCTTCCCGTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAAGTG	GGTTTGGCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	ACAACATGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240



TTCCGGGATT	GGGTGTTATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTTGT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTTGAA	CAGATCCTTC	350
GGGAATTGAG	ACTTCAGGTC	AACTCCACGC	GCTTGGACCT	GTCCCTGACC	AAAGGATTAC	400
CCAATTGGAT	CTCCTCAGCA	TTTTCTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTTG	450
GAGATACACT	TTGCTGTGGA	TTAGTGTGTC	TTCTTTGATT	GCTCTGTAAG	CTTAAGGCCG	500
AAACTAGGAG	AGACAAGGTG	GTTATTGCCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	550
CCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TCGCTGGCCA	CTCAGCTCTT	ATATCCCATG	600
AGGCTAGTCT	CATTGCACGG	GATAGAGTGA	GTGTGCTTCA	GCAGCCCGAG	AGAATTGCAC	650
GGCTAAGCAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	700
TCATCTTTCA	AGAAGGTTGA	GTGTCCAAGT	GTCCTTCCTC	CAGGCAAAAC	GACACGGGAG	750
CAGGTACGGG	TTGCTCTGGG	TAAAAGCCTG	TGAGCCTAAG	AGCTAATCCT	GTACATGGCT	800
CCTTTACCTA	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	850
ATTTGCTCTT	ATTAAAAGGA	AAGGGGGAGA	TGTTGGGAGC	CGCGCCACA	TTCGCCGTTA	900
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGCGC	ATGCGCCGAG	950
GGTGGTTCTT	CACTCCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1000
CAGTCAATCA	GGGAGTGACA	CGTCCTAGGC	GAAGGAAAAAT	TCTCCTTAAT	AGGGACGGGG	1050
TTTCGTTTTT	TCTCTCTCTT	GCTTCGCTCT	CTCTTGCTTC	TTGCTCTCTT	TTCCTGAAGA	1100
TGTAAGAATA	AAGCTTTGCC	GCAGAAGATT	CTGGTCTGTG	GTGTTCTTCC	TGGCCGCTCG	1150
TGAGAACGCG	TCTAATAACA	ATTGGTGCCG	AAACCCGGGT	GATAATGATT	ATCATCTACA	1200
TATCACAAAC	TGCGTGGAGG					1250

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	ACTTTACGGG	TCCTTTCACAT	50
ACAACCTGCCA	CGAGGCCCCG	TGCTCTGGTA	ATAGATCTTT	GCTGAAAAGG	CACACACATG	100
ACACATTACT	CAAGGTGGGC	TCATCTGAGC	TGCAGATTCA	GCTTAATATG	AATCTTGCCA	150
ATTGTGTGAA	ATCATAAATC	TTCAAAGTGA	CACTCATTGC	CAGACACAGG	TGCCCCACCTT	200
TGGCATAATA	AACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	250
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTTGAGAGCT	TAAATTTAAT	AAAGTGATAT	300
ACCTAATAAA	AATTAAATTA	AGAAGGTGTG	AATATACTAC	AGTAGGTAAA	TTATTTTCATT	350
AATTTATTTT	CTTTCTTAAT	CCTTTATAAT	GTTTTCTGCT	ATTGTCAATT	GCACATCCAT	400
ATGTTCAATT	CTTCACTGTA	ATGAAGAAAT	GTAGTAAATA	TACTTTCCGA	ACAAGTTGTA	450
TCAAATATGT	TACACTTGAT	TCCGTGTGTT	ACTTATCATT	TTATTATTAT	ATTGATTGCA	500
TTCTTTCGTT	ACTTGATATT	ATTACAAGGT	ACATATTTAT	TCTCTCAGAT	CTTCATTATA	550
CTCTAACCAT	TTTATAACAT	ACTTTATTTA	TTCAATTTCTT	ATGTGTGCTG	TGAGGCACAA	600
ATGCCAGAGA	GAACCTGAGC	AGATAAGAGG	ACAAATTGCA	AGAGTCAGTT	ACCTCCTGCT	650
GTTCTTGGA	AACTCAGGAT	CAAATTCAGG	TTGTCAGGCT	TGGCAGCATG	CACTTTTTCAC	700
CAGTGCCTCC	ATCTTGCTAG	CCCTGAACAT	CAAGCTTTGC	AGACAGACAG	GCTACACTAA	750
GTGAACGGT	CATTCACAGC	ATGCATGGTG	ATTTATTGTT	ACTTTCTATT	CCATGCCTTT	800
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTTTCGAGA	TAGAAGTTAC	TGAAAGAAAA	850
TTACATTGTT	TTCTATAGAT	CCTTGATACT	CTTTCAGCAG	ATATAGAGTT	TTAATCAGGT	900
CCTAGACCTT	TTCTTCACTC	TTATTAAATA	CTAAGTACAA	ATTAAGTTTA	TCCAAAACAG	950
TACGGATGTT	GATTTTGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1000
CACTTATTGG	GAATGTTTTT	GTTAATAAAA	GATTCAGGTG	TTACTCTAGG	TCAAGAGAAT	1050
ATTAAACATC	AGTCCCAAAT	TACAAACTTC	AATAAAAGAT	TTGACTCTCC	AGTGGTGGCA	1100
ATATAAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACGT	GCGTGGAGG		1150

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCCCT	ATCCCTAATC	CAGATTGGTG	GAATAACTTG	GTATAGATGT	TTGTGCATTA	60
AAAACCCTGT	AGGATCTTCA	CTCTAGGTCA	CTGTTTCAGCA	CTGGAACCTG	AATTGTGGCC	120
CTGAGTGATA	GGTCCTGGGA	CATATGCAGT	TCTGCACAGA	CAGACAGACA	GACAGACAGA	180
CAGACAGACA	GACAGACGTT	ACAAACAAAC	ACGTTGAGCC	GTGTGCCAAC	ACACACACAA	240
ACACCACTCT	GGCCATAAAT	ATTGAGGACG	TTGATTTATT	ATTCTGTGTT	TGTGAGTCTG	300
TCTGTCTGTC	TGTCTGTCTG	TCTGTCTGTC	TATCAAACCA	AAAGAAACCA	AACAATTATG	360
CCTGCCTGCC	TGCCTGCCTG	CCTACACAGA	GAAATGATTT	CTTCAATCAA	TCTAAAACGA	420
CCTCCTAAGT	TTGCCTTTTT	TCTCTTTCTT	TATCTTTTTT	TTTTTCTTTT	TCTTCTTCCT	480
TCCTTCCTTC	CTTCCTTCCT	TCCTTCCTTT	CTTCTTTTCT	TTCTTTCTTT	CTTACTTTCT	540
TTCTTTCTTT	CTTACATTTA	TTCTTTTCAT	ACATAGTTTC	TTAGTGTAAG	CATCCCTGAC	600
TGTCTTGAAG	ACACTTTGTA	GGCCTCAATC	CTGTAAGAGC	CTTCCTCTGC	TTTTCAAATG	660
CTGGCATGAA	TGTTGTACCT	CACTATGACC	AGCTTAGTCT	TCAAGTCTGA	GTTACTGGAA	720
AGGAGTTCCA	AGAAGACTGG	TTATATTTTT	CATTTATTAT	TGCATTTTAA	TTAAAATTTA	780
ATTTACCAA	AAGAATTTAG	ACTGACCAAT	TCAGAGTCTG	CCGTTTAAAA	GCATAAGGAA	840
AAAGTAGGAG	AAAAACGTGA	GGCTGTCTGT	GGATGGTCGA	GGCTGCTTTA	GGGAGCCTCG	900
TCACCATTCT	GCACTTGCAA	ACCGGGCCAC	TAGAACCCGG	TGAAGGGAGA	AACCAAAGCG	960
ACCTGGA AAC	AATAGGTCAC	ATGAAGGCCA	GCCACCTCCA	TCTTGTTGTG	CGGGAGTTCA	1020
GTTAGCAGAC	AAGATGGCTG	CCATGCACAT	GTTGTCTTTC	AGCTTGGTGA	GGTCAAAGTA	1080
CAACCGAGTC	ACAGAACAAG	GAAGTATACA	CAGTGAGTTC	CAGGTCAGCC	AGAGTTTACA	1140
CAGAGAAACC	ACATCTTGAA	AAAAACAAAA	AAATAAATTA	AATAAATATA	ATTTAAAAAT	1200
TTAAAAATAG	CCGGGAGTGA	TGGCGCATGT	CTTTAATCCC	AGCTCTCTTC	AGGCAGAGAT	1260
GGGAGGATTT	CTGAGTTTGA	GGCCAGCCTG	GCTGCAAAAG	TGAGTTCCAG	GACAGTCAGG	1320
GCTATACAGA	GA AACCTGT	CTTGAAAAC	AAACTAAAT	AACTAAACT	AACTAAAAA	1380
AATATAAAAT	AAAAATTTTA	AAGAATTTTA	AAAAACTACA	GAAATCAAAC	ATAAGCCCAC	1440
GAGATGGCAA	GTA ACTGCAA	TCATAGCAGA	AATATTATAC	ACACACACAC	ACACAGACTC	1500
TGTCATAAAA	TCCAATGTGC	CTTCATGATG	ATCAAATTTT	GATAGTCAGT	AATACTAGAA	1560
GAATCATATG	TCTGAAAATA	AAAGCCAGAA	CCTTTTCTGC	TTTTGTTTTC	TTTTGCCCCA	1620
AGATAGGGTT	TCTCTCAGTG	TATCCCTGGC	ATCCCTGCCT	GGA ACTTCCT	TTGTAGGTTT	1680
GGTAGCCTCA	AATCAGAGA	GGTCTCTCT	GCTGCTCTGC	CTGCCTGCCT	GCCTGCCTGC	1740
CTGCCTGCCT	GCCTGCCTCA	CTTCTTCTGC	CACCCACACA	ACCGAGTCGA	ACCTAGGATC	1800
TTTATTTCTT	TCTCTTTCTC	TCTTCTTTCT	TTCTTTCTTT	CTTTCTTTCT	TTCTTTCTTT	1860
CTTTCTTTCT	TTCTTATTCA	ATTAGTTTTT	AATGTAAGTG	TGTGTTTGTG	CTCTATCTGC	1920
TGCCTATAGG	CCTGTTGCC	AGGAGAGGGC	AACAGAACTT	AGGAGAAACC	ACCATGCAGC	1980
TCCTGAGAAT	AAGTGAAAAA	ACAACAAAAA	AAGGAAATTC	TAATCACATA	GAATGTAGAT	2040
ATATGCCGAG	GCTGTCAGAG	TGCTTTTAA	GGCTTAGTGT	AAGTAATGAA	AATTGTTGTG	2100
TGTCTTTTAT	CCAAACACAG	AAGAGAGGTG	GCTCGGCCCT	CATGTCGTGT	GTCTGCATGT	2160
AGACCAGGCT	GGCCTTGAAC	ACATTAATCT	GTCTGCCTCT	GCTTCCCTAA	TGCTGCGATT	2220
AAAGGCATGT	GCCACCACTG	CCCGGACTGA	TTCTTCTTTT	TTTTTTTTTT	TGGAAAATAC	2280
CTTTCTTTCT	TTTTCTCTCT	CTCTTTCTTC	CTTCTTCTCT	TTCTTTCTAT	TCTTTTTTTC	2340
TTTCTTTTTT	CTTTTTTTTT	TTTTTTTTTA	AATTTGCCTA	AGGTTAAAGG	TGTGCTCCAC	2400
AATTGCCTCA	GCTCTGCTCT	AATTCTCTTT	AAAAAAAAAAC	AAACAAAAAA	AAAACCAAAA	2460
CAGTATGTAT	GTATGTATAT	TTAGAAGAAA	TACTAATCCA	TTAATAACTC	TTTTTTCCTA	2520
AAATTCATGT	CATTCTTGTT	CCACAAAGTG	AGTTCCAGGA	CTTACCAGAG	AAACCTGTGT	2580
TTCAAATTTT	TGTGTTCAAG	GTCACCCCTG	CTTACAAAGT	GAGTTCCAAG	TCCGATAGGG	2640
CTACACAGAA	AAACCATATC	TCAGAAAAAA	AAAAAGTTCC	AAACACACAC	ACACACACAC	2700
ACACACACAC	ACACACACAC	ACACACACAC	ACACACACAG	CGCGCCGCGG	CGATGAGGGG	2760
AAGTCGTGCC	TAAAATAAAT	ATTTTCTTGG	CCAAAGTGAA	AGCAAATCAC	TATGAAGAGG	2820
TACTCCTAGA	ACAAACGGGC	TTTTTAATCA	TTCCAGCACT	TTCCAGCACT	GTTTAAATTT	2880
AACTCTGAAT	TTAGTCTTGG	AAAAGGGGGC	GGGTGTGGGT	GAGTGAGGGC	GAGCGAGCAG	2940
ACGGGCGGGC	GGGCGGGTGA	GTGGCCGGCG	GCGGTGGCAG	CGAGCACCAG	AAAACAACAA	3000
ACCCCAAGCG	GTAGAGTGTT	TTAAAAATGA	GACCTAAATG	TGGTGGAACG	GAGGTGCGCG	3060
CCACCCTCCT	CTTCCACTGC	TTAGATGCTC	CCTTCCCCTT	ACTGTGCTCC	CTTCCCCTAA	3120
CTGTGCCTAA	CTGTGCCTGT	TCCCTCACCC	CGCTGATTCG	CCAGCGACGT	ACTTTGACTT	3180

CAAGAACGAT	TTTGCCCTGTT	TTACACCGCTC	CCTGTGCATAC	TTTCGTTTTTT	GGGTGCECGA	3240
GTCTAGCCCG	TTCCGCTATGT	TCGGGCGGGA	CGATGGGGAC	CGTTTGTGCC	ACTCGGGAGA	3300
AGTGGTGGGT	GGGTACGCTG	CTCCGTCGTG	CGTGGGTGAG	TGCCGGAACC	TGAGCTCGGG	3360
AGACCCTCCG	GAGAGACAGA	ATGAGTGAGT	GAATGTGGCG	GCGCGTGACG	GATCTGTATT	3420
GGTTTGATG	GTTGATCGAG	ACCATTGTCC	GGCGACACCT	AGTGGTGACA	AGTTTCGGGA	3480
ACGCTCCAGG	CCTCTCAGGT	TGGTGACACA	GGAGAGGGAA	GTGCCTGTGG	TGAGGCGACC	3540
AGGGTGACAG	GAGGCCGGGC	AAGCAGGCGG	GAGCGTCTCG	GAGATGGTGT	CGTGTTTAAG	3600
GACGGTCTCT	AACAAGGAGG	TCGTACAGGG	AGATGGCCAA	AGCAGACCGA	GTTGCTGTAC	3660
GCCCTTTTGG	GA AAAATGCT	AGGGTTGGTG	GCAACGTTAC	TAGGTCGACC	AGAAGGCTTA	3720
AGTCCTACCC	CCCCCCCCCT	TTTTTTTTTT	TTTCCTCCAG	AAGCCCTCTC	TTGTCCCCGT	3780
CACCGGGGGC	ACCGTACATC	TGAGGCCGAG	AGGACGCGAT	GGGCCCCGGT	TCCAAGCCCG	3840
TGTGGCTCGG	CCAGCTGGCG	CTTCGGGTCT	TTTTTTTTTT	TTTTTTTTTT	TTTTCCTCCA	3900
GAAGCCTTGT	CTGTGCTGT	CACCGGGGGC	GCTGTACTTC	TGAGGCCGAG	AGGACGCGAT	3960
GGGCCCCGGC	TTCCAAGCCG	GTGTGGCTCG	GCCAGCTGGA	GCTTCGGGTC	TTTTTTTTTT	4020
TTTTTTTTTT	TTTTTTTCTC	CAGAAGCCTT	GTCTGTGCGT	GTCACCGGGG	GCGCTGTACT	4080
TCTGAGGCCG	AGAGGACGCG	ATGGGTGCGC	TTCCAAGCCG	ATGTGGCGGG	GCCAGCTGGA	4140
GCTTCGGGTT	TTTTTTTTTT	CTCCAGAAGC	CCTCTCTTGT	CCCCCTCACC	GGGGGCGCTG	4200
TACTTCTGAG	GCCGAGAGGA	CGTGATGGGC	CCGGGTTCCT	GGCGGATGTC	GCCCGGTCAG	4260
CTGGAGCTTT	GGATCTTTTT	TTTTTTTTTT	CCTCCAGAAG	CCCTCTCTTG	TCCCCGTCAC	4320
CGGGGGCACC	TTACATCTGA	GGGCGAGAGG	ACGTGATGGG	TCCGCTTCC	AAGCCGATGT	4380
GGCGGGGCCA	GCTGGAGCTT	CGGGTTTTTT	TTTTTCTCTC	CAGAAGCCCT	CTCTTGTCCC	4440
CGTCACCGGG	GGCGCTGTAC	TTCTGAGGCC	GAGAGGACGT	GATGGGCCCC	GGTCCAGGCG	4500
GGATGTGCGC	CGGTACAGCTG	GAGCTTTGGA	TCATTTTTTT	TTTTCCCTCC	AGAAGCCCTC	4560
TCTTGTCCCC	GTCACCGGGG	GCACCGTACA	TCTGAGGCCG	AGAGGACACG	ATGGGCGCTG	4620
CTTCCAAGCC	GATGTGGCCC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	TTTTTTCCTC	4680
CAGAAGCCTT	GTCTGTGCGT	GTCACCCGGG	GCGCTGTACT	TCTGAGGCCG	AGAGGACGCG	4740
ATGGGCCCCG	CTTCCAAGCC	GGTGTGGCTC	GGCCAGCTGG	AGCTTCGGGT	CTTTTTTTTT	4800
TTTTTTTTTT	TTCTCCAGA	AACCTTGTCT	GTCGTGTCTA	CCCGGGGCGC	TTGTACTTCT	4860
GATGCCGAGA	GGACGCGATG	GGCCCGTCTT	CCAGGCCGAT	GTGGCCCGGT	CAGCTGGAGC	4920
TTTGGATCTT	TTTTTTTTTT	TTTCCCTCCA	GAAGCCCTCT	CTTGTCCCCG	TCACCGGGGG	4980
CACCTTACAT	CTGAGGCCCTA	GAGGACACGA	TGGGCCCGGG	TTCCAGGCCG	ATGTGGCCCC	5040
GTCAGCTGGA	GCTTTGGATC	TTTTTTTTTT	TTTTCTTCCA	GAAGCCCTCT	TGTCCCCGTC	5100
ACCGGTGGCA	CTGTACATCT	GAGGCGGAGA	GGACATTATG	GGCCCGGCTT	CCAATCCGAT	5160
GTGGCCCCGT	CAGCTGGAGC	TTTGGATCTT	ATTTTTTTTT	TAATTTTTTT	TTCCAGAAGC	5220
CCTCTTGTCC	CTGTACCCGG	TGGCACGGTA	CATCTGAGGC	CGAGAGGACA	TTATGGGCCCT	5280
GGCTTCCAGG	CCGATGTGGC	CCGGTCAGCT	GGAGCTTTGG	ATCTTTTTTT	TTTTTTTTTT	5340
TTTTTCTCTC	AGAAGCCCTC	TCTGTCCCTG	TCACCGGGGG	CCCTGTACGT	CTGAGGCCGA	5400
GGGAAAGCTA	TGGGCGCGGT	TTTCTTTTAT	TGACCTGTCT	GTCTTATCAG	TTCTCCGGGT	5460
TGTACGGGTC	GACCAAGTTG	TCCTTTGAGG	TCCGGTTCTT	TTCGTTATGG	GGTCATTTTT	5520
GGGCCACCTC	CCCAGGTATG	ACTTCCAGGC	GTCGTTGCTC	GCCTGTCACT	TTCTCCCTGA	5580
TCTCTTTTAT	GCTTGTGATC	TTTTCTATCT	GTTCTTATTG	GACCTGGAGA	TAGGTACTGA	5640
CACGCTGTCC	TTTCCCTATT	AACACTAAAG	GACACTATAA	AGAGACCCTT	TGCATTTAAG	5700
GCTGTTTTCG	TTGTCCAGCC	TATTCTTTTT	ACTGGCTTGG	GTCTGTGCGG	GTGCCTGAAG	5760
CTGTCCCCGA	GCCACGCTTC	CTGCTTTCCC	GGGCTTGCTG	CTTGCGTGTG	CTTGCTGTGG	5820
GCAGCTTGTG	ACAACCTGGG	GCTGTGACTT	TGCTGCGTGT	CAGACGTTTT	TCCCGATTTT	5880
CCCGAGGTGT	CGTTGTACAC	CCTGTCCCCG	TTGGAATGGT	GGAGCCAGCT	GTGGTTGAGG	5940
GCCACCTTAT	TTCCGGCTCAC	TTTTTTTTTT	TTTTTTTCTC	TTGGAGTCCC	GAACCTCCGC	6000
TCTTTTCTCT	TCCCGGTCTT	TCTTCCACAT	GCCTCCCGAG	TGCATTTCTT	TTTGTTTTTT	6060
TTCTTTTTTT	TTTTTTTTTT	TTGGGGAGGT	GGAGAGTCCC	GAGTACTTCA	CTCCTGTCTG	6120
TGGTGTCCAA	GTGTTTCATG	CACGTGCCCT	CCGAGTGCAC	TTTTTTTTTG	GGCAGTCGCT	6180
CGTTGTGTTT	TCTTGTCTGT	TGTCTGCCCG	TATCAGTAAC	TGTCTTGCCC	CGCGTGTAAG	6240
ACATTCTTAT	CTCGCTTGT	TCTCCCGATT	GCGCGTCGTT	GCTCACTCTT	AGATCGATGT	6300
GGTGCTCCGG	AGTTCTCTTC	GGGCCAGGGC	CAAGCCGCGC	CAGGCGAGGG	ACGGACATTC	6360
ATGGCGAATG	GCGGCCGCTC	TTCTCGTTCT	GCCAGCGGGC	CCTCGTCTCT	CCACCCCATC	6420
CGTCTGCCGG	TGGTGTGTGG	AAGGCAGGGG	TGCGGCTCTC	CGGCCCCGAC	CTGCCCCGCG	6480
CGCACTTTTC	TCAGTGGTTC	GCGTGGTCCT	TGTGGATGTG	TGAGGCGCCC	GGTTGTGCCC	6540
TCACGTGTTT	CACTTTGGTC	GTGTCTCGCT	TGACCATGTT	CCCAGAGTCG	GTGGATGTGG	6600
CCGGTGGCGT	TGCATACCTT	TCCCGTCTGG	TGTGTGCACG	CGCTGTTTCT	TGTAAGCGTC	6660
GAGGTGCTCC	TGGAGCGTTC	CAGGTTTGTG	TCTAGGTGTC	CTGCTTCTGA	GCTGGTGGTG	6720
GCGCTCCCCA	TTCCCTGGTG	TGCCTCCGGT	GCTCCGTCTG	GCTGTGTGCC	TTCCCGTTTG	6780
TGTCTGAGAA	GCCCGTGAGA	GGGGGGTCTGA	GGAGAGAAGG	AGGGGCAAGA	CCCCCTTCT	6840
TCGTGCGGTG	AGGCGCCAC	CCCGCGACTA	GTACGCCTGT	GCGTAGGGCT	GGTGCTGAGC	6900
GGTCGCGGCT	GCGGTGGA	AGTTTCTCGA	GAGACTCATT	GCTTTCCCGT	GGGGAGCTTT	6960
GAGAGGCCTG	GCTTTCGGGG	GGGACCGGTT	GCAGGTTCTC	CCCTGTCCGC	GGATGCTCAG	7020
AATGCCCTTG	GAAGAGAACC	TTCTGTGTC	CGCAGACCCC	CCGCGCGGCT	CGCCCCGCTG	7080

TTGGTCTTCT	GGTTTCCCTG	TGTGCTCGTC	GCATGCATCC	TCTCTCGGTG	GCCGGGGGTC	7140
GTCGGGGTTF	TGGGTCCGTC	CCGCCCTCAG	TGAGAAAGTT	TCCTTCTCTA	GCTATCTTCC	7200
GGAAAGGGTG	CGGGCTTCTT	ACGGTCTCGA	GGGGTCTCTC	CCGAATGGTC	CCCTGGAGGG	7260
CTCGCCCCCT	GACCGCCTCC	CGCGCGCGCA	GCCTTTGCTC	TCTCGTCTAC	CGCGGCCCGC	7320
GGCCTCCCCG	CTCCGAGTTC	GGGGAGGGAT	CACGCGGGGC	AGAGCCTGTC	TGTGCTCCTG	7380
CCGTTGCTGC	GGAGCATGTG	GCTCGGCTTG	TGTGTTGTTT	GGCTGCGGAG	AGGGCTCCGT	7440
GCACACCCCC	GCGTGCGCGT	ACTTTCCCTC	CCTCCTGAGG	GCCGCGGTGC	GGACGGGGTG	7500
TGGGTAGGCG	ACGGTGGGCT	CCCGGGTCCC	CACCGCTCTT	CCCGTGCTTC	ACCCGTGCCCT	7560
TCCGTGCGGT	GCGTCCCTCT	CGCTCGCGTC	CACGACTTTG	GCGGCTCCCG	CGACGGCGGC	7620
CTGCGCCGCG	CGTGGTGCGT	GCTGTGTGCT	TCTCGGGCTG	TGTGTTTGTG	TGCGCTCGCC	7680
CCCCCTTCC	CGCGGCAGCG	TTCCACGGC	TGGCGAAATC	GCGGGAGTCC	TCCTTCCCCT	7740
CCTCGGGGTC	GAGAGGGTCC	GTGTCTGGCG	TTGATTGATC	TGCTCTCGG	GGACGGGACC	7800
GTTCTGTGGG	AGAACGGCTG	TTGGCCCGGT	CCGGCGCGAC	GTCGACGTG	GGGACCCACT	7860
GCCGCTCGGG	GGTCTTCGTC	GGTAGGCATC	GGTGTGTCCG	CATCGTCTC	TCTCTCGTGT	7920
CGGTGTGCGC	TCCTCGGGCT	CCCGGGGGGC	CGTCGTGTTT	CGGGTCGGCT	CGGCGCTGCA	7980
GGTGTGGTGG	GA CTGCTCAG	GGGAGTGGTG	CAGTGTGATT	CCCGCCGGTT	TTGCCTCGCG	8040
TGCCCTGACC	GGTCCGACGC	CCGAGCGGTC	TCTCGGTCCC	TTGTGAGGAC	CCCCTTCCGG	8100
GAGGGGCCCC	TTTCGGCCCG	CCTTGCCGTC	GTCGCCGGCC	CTCGTCTGTC	TGTGCTGTTT	8160
CCCCCTCCCC	GCTCGCCGCA	GCCGGTCTTT	TTTCTCTCTT	CCCCCTCTCT	CCTCTGACTG	8220
ACCCGTGGCC	GTGCTGTGCG	ACCCCCGCA	TGGGGCGGCG	CGGGCACGTA	CGCGTCCGGG	8280
CGGTCAACCG	GGTCTTGGGG	GGGGGCCGAG	GGGTAAGAAA	GTCGGCTCGG	CGGGCGGGAG	8340
GAGCTGTGGT	TTGGAGGGCG	TCCCGGCCCC	CGCGCCGTGG	CGGTGTCTTG	CGCGTCTTTG	8400
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ATTAGTTGGA	CCAATTAGTT	GGCTGGTTTG	GGAGGTTTCT	TTTGTTCCTG	ATTTGGGTGT	21000
TTGTGGGGCT	GGGATCAGG	TATCTCAACG	GAATGCATGA	AGGTTAAGGT	GAGATGGCTC	21060
GATTTTGTGA	AAGATTACTT	TTCTTAGTCT	GAGGAAAAAA	TAAAATAATA	TTGGGCTACG	21120
TTTCATTGCT	TCATTCTAT	TTCTCTTTCT	TTCTTTCTTT	CTTTCAGATA	AGGAGGTCGG	21180
CCAGTTCCTC	CTGCCTTCTG	GAAGATGTAG	GCATTGCATT	GGGAAAAGCA	TTGTTTGAGA	21240
GATGTGCTAG	TGAACAGAG	AGTTTGGATG	TCAAGCCGTA	TAATGTTTAT	TACAATATAG	21300
AAAAGTTCTA	ACAAAGTGAT	CTTTAACTTT	TTTTTTTTTT	TTTCTCCTTC	TACTTCTACT	21360
TGTTCTCACT	CTGCCACCAA	CGCGCTTTGT	ACATTGAATG	TGAGCTTTGT	TTTGCTTAAC	21420
AGACATATAT	TTTTTCTTTT	GGTTTGTCTT	GACATGGTTT	CCCTTTCTAT	CCGTGCAGGG	21480
TTCCAGACG	GCCTTTTGAG	AATAAAATGG	GAGGCCAGAA	CCAAAGTCTT	TTGAATAAAG	21540
CACCACAAC	CTAACCTGTT	TGGCTGTTTT	CCTTCCCAAG	GCACAGATCT	TTCCAGCAT	21600
GGAAAAGCAT	GTAGCAGTTG	TAGGACACAC	TAGACGAGAG	CACCAGATCT	CATTGTGGGT	21660
GGTTGTGAAC	CACCCACCAT	GTGGTTGCCT	GGGATTTGAA	CTCAGGATCT	TCAGAAGACG	21720
AGTCAGGGCT	CTAAACCGAT	GAGCCATCTC	TCCAGCCCTC	CTACATTCCT	CTTAAGGCA	21780
TGAATGATCC	CAGCATGGGA	AGACAGTCTG	CCCTCTTTGT	GGTATATCAC	CATATACTCA	21840
ATAAAATAAT	GAAATGAATG	AAGTCTCCAC	GTATTTATTT	CTTCGAGCTA	TCTAAATTCT	21900
CTCACAGCAC	CTCCCCCTCC	CCCACACTGC	CTTCTCCCT	ATGTTTGGGT	GGGGCTGGGG	21960
GAGGGGTGGG	GTGGGGGCAG	GGATCTGCAT	GTCTTCTTGC	AGGTCTGTGA	ACTATTTGCG	22020
ATGGCCTGGT	TCTCTGAACT	GTTGAGCCTT	GTCTATCCAG	AGGCTGACTG	GCTAGTTTTT	22080
TACCTGAAGT	CCCTGAGTGA	TGATTTCCCT	GTGAATTC			22118

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGACACGC	TGTCCTCTGG	CGACCTGTGG	TCGGAGAGGT	TGGGCCTCCG	GATGCGCGCG	60
GGGCTCTGGC	CTCACGGTGA	CCGGCTAGCC	GGCCGCGCTC	CTGCCTTGA	CCGCCTGCCG	120
CGGCCCGCGG	GCCTGCTGTT	CTCTCGCGCG	TCCGAGCGTC	CCGACTCCCG	GTGCCGCGCC	180
GGGTCCGGGT	CTCTGACCCA	CCCGGGGGCG	GCGGGGAAGG	CGGCGAGGGC	CACCGTGCCC	240
CGTGCGTCT	CCGCTGCGGG	CGCCCGGGCG	GCCGCACAAC	CCCACCCGCT	GGCTCCGTGC	300
CGTGCGTGTC	AGGCGTTCTC	GTCTCCGCGG	GGTTGTCCGC	CGCCCCCTTC	CCGGAGTGGG	360
GGGTGGCCGG	AGCCGATCGG	CTCGCTGGCC	GGCCGGCCTC	CGCTCCCGGG	GGGCTCTTCG	420
ATCGATGTGG	TGACGTCTGT	CTCTCCCGGG	CCGGGTCCGA	GCCGCGACGG	GCGAGGGGCG	480
GACGTTCTGT	GCGAACGGGA	CCGTCTTTCT	CGCTCCGCCC	GCGCGGTCCC	CTCGTCTGCT	540
CCTCTCCCCG	CCCGCCGGCC	GGCGTGTGGG	AAGGCGTGGG	GTGCGGACCC	CGGCCCGACC	600
TCGCCGTCCC	GCCCGCCGCC	TTCGCTTCGC	GGGTGCGGGC	CGGCGGGGTC	CTCTGACGCG	660
GCAGACAGCC	CTGCCTGTCT	CCTCCAGTGG	TTGTGCACTT	GCGGGCGGCC	CCCCCTCCGCG	720
GCGGTGGGGG	TGCCGTCCCC	CCGGCCCGTC	GTGCTGCCCT	CTCGGGGGGG	GTTTGCGCGA	780
GCGTCGGCTC	CGCCTGGGCC	CTTGCGGTGC	TCCTGGAGCG	CTCCGGGTTG	TCCCTCAGGT	840
GCCCGAGGCC	GAACGGTGGT	GTGTCGTTCC	CGCCCCCGGC	GCCCCCTCCT	CCGGTCGCGG	900
CCGCGGTGTC	CGCGCGTGGG	TCCTGAGGGA	GCTCGTCGGT	GTGGGGTTTC	AGGCGGTTTG	960
AGTGAGACGA	GACGAGACGC	GCCCCCTCCA	CGCGGGGAAG	GGCGCCCGCC	TGCTCTCGGT	1020
GAGCGCACGT	CCCGTGCTCC	CCTCTGGCGG	GTGCGCGCGG	GCCGTGTGAG	CGATCGCGGT	1080
GGGTTCGGGC	CGGTGTGACG	CGTGCGCCCG	CCGGCCCGCC	AGGGGCTGCC	GTTCTGCCTC	1140
CGACCGGTCT	TGTGTGGGTT	GACTTCGGAG	GCGCTCTGCC	TCGGAAGGAA	GGAGGTGGGT	1200
GGACGGGGGG	GCCTGGTGGG	GTTGCGCGCA	CGCGCGCACC	GGCCGGGCCC	CCGCCCTGAA	1260
CGCGAACGCT	CGAGGTGGCC	GCGCGCAGGT	GTTTCTCGGT	ACCGCAGGGC	CCCCTCCCTT	1320
CCCCAGGCGT	CCCTCGGCGC	CTCTGCGGGC	CCGAGGAGGA	GCGGCTGGCG	GGTGGGGGGA	1380
GTGTGACCCA	CCCTCGGTGA	GAAAAGCCTT	CTCTAGCGAT	CTGAGAGGCG	TGCCTTGGGG	1440
GTACCGGATC	CCCCGGGCCG	CCGCCTCTGT	CTCTGCCTCC	GTTATGGTAG	CGCTGCCGTA	1500
GCGACCCGCT	CGCAGAGGAC	CCTCCTCCGC	TTCCCCCTCG	ACGGGGTTGG	GGGGGAGAAG	1560
CGAGGGTTCC	GCCGGCCACC	GCGGTGGTGG	CCGAGTGCGG	CTCGTCGCCT	ACTGTGGCCC	1620
GCGCCTCCCC	CTTCCGAGTC	GGGGGAGGAT	CCCGCCGGGC	CGGGCCCGGC	GCTCCCAACC	1680
AGCGGGTTGG	GACGCGGGCG	CCGGCGGGCG	GTGGGTGTGC	GCGCCCGGCG	CTCTGTCCCG	1740
CGCGTGACCC	CCTCCGTCCG	CGAGTCGGCT	CTCCGCCCGC	TCCCGTGCCG	AGTCGTGACC	1800
GGTGCCGACG	ACCGCGTTTG	CGTGGCACGG	GGTCGGGCCC	GCCTGGCCCT	GGGAAAGCGT	1860
CCCACGGTGG	GGGCGCGCCG	GTCTCCCGGA	GCGGGACCGG	GTCGGAGGAT	GGACGAGAAT	1920
CACGAGCGAG	GGTGTGGTG	GCGTGTCCGG	TTCGTGGCTG	CGGTCTGCTC	GGGGCCCCCG	1980
GTGGCGGGGC	CCCGGGGCTC	GCGAGGCGGT	TCTCGGTGGG	GGCCGAGGGC	CGTCCGGCGT	2040
CCCAGGCGGG	GCGCCGCGGG	ACCGCCCTCG	TGTCTGTGGC	GGTGGGATCC	CGCGGCCCGT	2100
TTTTCTTGGT	GGCCCGGCCG	TGCCTGAGGT	TTCTCCCCGA	GCCGCCGCCT	CTGCGGGCTC	2160
CCGGGTGCCC	TTGCCCTCGC	GGTCCCCCGC	CCTCGCCCGT	CTGTGCCCTC	TTCCCCGCCC	2220
GCCGCCCGCC	GATCCTCTTC	TTCCCCCGCA	GCGGCTCACC	GGCTTCACGT	CCGTGTGTGG	2280
CCCCGCCTGG	GACCGAACC	GGCACCGCCT	CGTGGGGCGC	CGCCGCCGGC	CACTGATCGG	2340
CCCGGCGTCC	GCGTCCCCCG	GCGCGCGCCT	TGGGGACCGG	GTCGGTGGCG	CGCCGCGTGG	2400
GGCCCGGTGG	GCTTCCCCGA	GGGTTCGGGG	GGTCGGCCTG	CGGCGCGTGC	GGGGGAGGAG	2460
ACGGTTCCGG	GGGACCGGCC	GCGGCTGCGG	CGGCGGCGGT	GGTGGGGGGA	GCCGCGGGGA	2520
TCGCCGAGGG	CCGGTCGGCC	GCCCCGGGTG	CCCCCGGGTG	CCGCCGGCGG	CGGTGAGGCC	2580
CCGCGCGTGT	GTCCCGGCTG	CGGTGCGCCG	CGCTCGAGGG	GTCCCCGTGG	CGTCCCCCTT	2640
CCCGCCGGCC	GCCTTTCTCG	CGCCTTCCCC	GTCGCCCGCG	CCTCGCCCGT	GGTCTCTCGT	2700
CTTCTCCCGG	CCCGCTCTTC	CGAACCGGGT	CGGCGCGTCC	CCCGGGTGCG	CCTCGCTTCC	2760
CGGGCCTTGC	GCGGCCCTTC	CCCGAGGCGT	CCGTCCCAGG	CGTCGGCGTC	GGGGAGAGCC	2820
CGTCCTCCCC	GCGTGGCGTC	GCCCCGTTTC	GCGCGCGCGT	GCGCCCGAGC	GCGGCCCGGT	2880
GGTCCCTCCC	GGACAGGCGT	TCGTGCGACG	TGTGGCGTGG	GTCGACCTCC	GCCTTGCCGG	2940
TCGCTCGCCC	TCTCCCCGGG	TCGGGGGGTG	GGGCCCGGGC	CGGGGCCTCG	GCCCCGGTCC	3000
CTGCCTCCCG	TCCCGGGCGG	GGGCGGGCGC	GCCGGCCGGC	CTCGGTTCGC	CTCCCTTGGC	3060
CGTCGTGTGG	CGTGTGCCAC	CCCTGCGCGG	GCGCCCGCGG	GCGGGGCTCG	GAGCCGGGCT	3120
TCGGCCGGGC	CCCGGGCCCT	CGACCGGACC	GGCTGCGCGG	GCGCTGCGGC	GCGACGGCGC	3180
GACTGTCCCC	GGGCCGGGCA	CCGCGGTCCG	CCTCTCGCTC	GCCGCCCGGA	CGTCGGGGCC	3240
GCCCCGCGGG	GCGGGCGGAG	CGCCGTCCCC	GCCTCGCCGC	CGCCCGCGGG	CGCCGGCCGC	3300
GCGCGCGCGC	GCGTGGCCGC	CGGTCCCTCC	CGGCCCGCGG	GCGCGGGTCG	GGCCGTCCCG	3360
CTCCTCGCGG	GCGGGCGCGA	CGAAGAAGCG	TCGCGGGTCT	GTGGCGCGGG	GCCCCCGGTG	3420



GTGCTGTGCG	GTGGGGGGGG	GCTGGTTGGG	GCTGCGGTTT	GGGCGGGGGG	GGGCGGGGGG	3480
CCACCGGTTC	GGGCGGGGGG	GGGCGGGGGG	GCTGCGGTTT	GGGCGGGGGG	GGGCGGGGGG	3540
CCGCTGCGTC	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	3600
AGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	3660
TGGTTGATCC	TGGCAGTAGC	ATATGCTTGT	CTCAAAGATT	AAGCCATGCA	TGTCTAAGTA	3720
CGCACGGCCG	GTACAGTGAA	ACTGCGAATG	GCTCATTAAG	TCAGTTATGG	TGCTTTGGGT	3780
CGTTCGCTCC	TCTCTTACTT	GGATAACTGT	GCTAATTCTA	GAGCTAATAC	ATGCCGACGG	3840
GCGCTGACCC	CCTTCGCGGG	GGGGATGCGT	GCAATTTATC	GATCAAAACC	AACCGGCTCA	3900
GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	GGGCGGGGGG	3960
TCGGGGCGAT	CGCACGGGGG	CGGTGGCGGG	GACGACCCAT	TCGAACGTCT	GCCCTATCAA	4020
CTTTCGATGG	TAGTCGCGGT	GCCTACCATG	GTGACCACGG	GTGACGGGGA	ATCAGGGTTC	4080
GATTCCGGAG	AGGGAGCCTG	AGAAACGGCT	ACCACATCCA	AGGAAGGCGG	CAGGCGCGCA	4140
AATTACCCAC	TCCCGACCCG	GGGAGGTAGT	GACGAAAAAT	AACAATACAG	GACTCTTTTC	4200
AGGCCCTGTA	ATTGGAATGA	GTCCACTTTA	AATCCTTTAA	CGAGGATCCA	TTGGAGGGCA	4260
AGTCTGGTGC	CAGCAGCCGC	GGTAATTCCA	GCTCCAATAG	CGTATATTAA	AGTTGCTGCA	4320
GTTAAAAAGC	TCGTAGTTGG	ATCTTGGGAG	CGGGCGGGCG	GTCCGCCGCG	AGGCGAGCCA	4380
CCGCCCCGTC	CCGCCCCCTG	CCTCTCGGCG	CCCCCTCGAT	GCTCTTAGCT	GAGTGTCCCC	4440
CGGGGGCCGA	AGCGTTTACT	TTGAAAAAAT	TAGAGTGTTT	AAAGCAGGCC	CGAGCCGCCT	4500
GGATACCGCA	GCTAGGAATA	ATGGAATAGG	ACCAGCGTTC	TATTTTGTTC	GTTTTTCGAA	4560
CTGAGGCCAT	GATTAAGAGG	GACGGCCGGG	GGCATTTCGT	TTGCGCCGCT	AGAGGTGAAA	4620
TTCTTGGACC	GGCGCAAGAC	GGACCAGAGC	GAAAGCATTT	GCCAAGAATG	TTTTTCATTAA	4680
TCAAGAACGA	AAGTCGGAGG	TTCGAAGACG	ATCAGATACC	GTCTAGTTTC	CGACCATAAA	4740
CGATGCCGAC	CGGCGATGCG	CGGCGTTTAT	TCCCATGACC	CGCCGGGCGG	CTTCCGGGAA	4800
ACCAAAGTCT	TTGGGTTCCG	GGGGGAGTAT	GGTTGCAAGG	CTGAAACTTA	AAGGAATTGA	4860
CGGAAGGGCA	CCACCAGGAG	TGGAGCCTGC	GGCTTAATTT	GACTCAACAC	GGGAAACCTC	4920
ACCCGGCCCC	GACACGGACA	GGATTGACAG	ATTGATAGCT	CTTTCTCGAT	TCCGTGGGTG	4980
GTGGTGCTAG	GCCGTTCTTA	GTGGGTGGAG	CGATTTGTCT	GCTTAATTCC	GATAACGAAC	5040
GAGACTCTGG	CATGCTAACT	AGTTACGCGA	CCCCCGAGCG	GTGCGCGTCC	CCCAACTTCT	5100
TAGAGGGACA	AGTGGCGTTC	AGCCACCCGA	GATTGAGCAA	TAACAGGTCT	GTGATGCCCT	5160
TAGATGTCCG	GGGCTGCACG	CGCGCTACAC	TGACTGGCTC	AGCGTGTGCC	TACCTACGCG	5220
CGGCAGGCGC	GGGTAACCCG	TTGAACCCCA	TTGCTGATGG	GGATCGGGGA	TTGCAATTAT	5280
TCCCCATGAA	CGAGGGAATT	CCCGAGTAAG	TGCGGGTCAT	AAGCTTGCGT	TGATTAAGTC	5340
CCTGCCCTTT	GTACACACCG	CCCGTCGCTA	CTACCGATTG	GATGGTTTAG	TGAGGCCCTC	5400
GGATCGGCCC	CGCCGGGGTC	GGCCACCGGC	CCTGGCGGAG	CGCTGAGAA	ACGGTCAAGC	5460
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ATCATTAACG	GAGCCCGGAG	GGCGAGGCCC	GCGGCGGCGC	CGCCGCGGCC	GCGCGCTTCC	5580
CTCCGCACAC	CCACCCCCCG	ACCAGCAGCG	CGGCGGTGCG	CGGCGGGGGG	CGGCGGGGGG	5640
GTTTCGTTCC	TCGCTCGTTC	GTTCGCGGCC	CGGCCCCGCC	GCCGCGAGAG	CCGAGAACTC	5700
GGGAGGGAGA	CGGGGGGGAG	AGAGAGAGAG	AGAGAGAGAG	AGAGAGAGAG	AGAGAGAGAA	5760
AGAAGGGCGT	GTGCTTGGTG	TGCGCGTGTC	GTGGGGCCGG	CGGGCGGGCG	GGAGCGGTCC	5820
CCGGCCGCGG	CCCCGACGAC	GTGGGTGTCT	CGGGCGGGCG	GGGCGGTTC	CGGCGGCGTC	5880
GCGGCGGGTC	TGGGGGGGTC	TCGGTGCCCT	CCTCCCCGCC	GGGGCCCGTC	GTCCGGCCCC	5940
GCCGCGCCGG	CTCCCCGTCT	TCGGGGCCGG	CCGATTTCCT	GTGCGCTCCG	CCGCGCCGCT	6000
CCGCGCCGCC	GGGCACGGCC	CCGCTCGCTC	TCCCCGGCCT	TCCCGCTAGG	GCGTCTCGAG	6060
GGTCCGGGGG	CGGACGCCGG	TCCCCCTCCC	CGCCTCCTCG	TCCGCCCCCG	CGCCGTCCAG	6120
GTACCTAGCG	CGTTCCGGCG	CGGAGGTTTA	AAGACCCCTT	GGGGGGATCG	CCCGTCCGCC	6180
CGTGGGTCCG	GGGCGGTGGT	GGGCCCCGCG	GGGAGTCCCG	TCGGGAGGGG	CCCGGCCCTC	6240
CCGCGCGCTC	CACCGCGGAC	TCCGCTCCCC	GGCCGGGGCC	GCGCCGCGCG	CGCCGCCGCG	6300
GCGGCGGTCG	GGTGGGGGCT	TTACCCGGCG	GCGGCGGCTG	GGGGTGGTGT	CCGCGCTCGC	6360
GCGCCCCCGG	CCGTGGGGGG	GGGAACCCCG	GGGCGGCTGT	GGGGTGGTGT	CCGCGCTCGC	6420
CCCCGCGTGG	CGGGCGGCGC	CCTCCCCGTG	GTGTGAAACC	TTCCGACCCC	TCTCCGGAGT	6480
CCGCTCCCGT	TTGCTGTCTC	GTCTGGCCGG	CCTGAGGCAA	CCCCCTCTCC	TCTTGGGCGG	6540
GGGGGGCGGG	GGGACGTGCC	GCGCCAGGAA	GGGCTCCTCT	CCGGTGCGTC	GTGCGGAGCG	6600
CCCTCGCCAA	ATCGACCTCG	TACGACTCTT	AGCGGTGGAT	CACTCGGCTC	GTGCGTCTGAT	6660
GAAGAACGCA	GCTAGCTGCG	AGAATTAATG	TGAATTGCAG	GACACATTGA	TCATCGACAC	6720
TTCGAACGCA	CTTGCGGGCC	CGGGTTCCCT	CGGGGCTAC	GCCTGTCTGA	GCGTCTGTTG	6780
CCGATCAATC	CCCCCGGGGG	TGCTTCCGGG	CTCCTCGGGG	TGCGCGGCTG	GGGGTTCCTT	6840
CGCAGGGCCC	GCCGGGGGCC	CTCCGTCCCC	CTAAGCGCAG	ACCCGGCGGC	GTCCGCCCTC	6900
CTCTTGCCGC	CGCGCCCGCC	CCTTCCCCCT	CCCCCGCGCG	GCCCTGCGTG	GTCACGCGTC	6960
GGGTGGCGGG	GGGAGAGGGG	GGGCGCGCCC	GGCTGAGAGA	GACGGGGAGG	GCGGCGCCCG	7020
CGCCGGAAGA	CGGAGAGGGA	AAGAGAGAGC	CGGCTCGGGC	CGAGTTCCCG	TGGGCTCCCG	7080
CTGCGGTCCG	GGTTCTCTCC	TCGGGGGGCT	CCCTCGCGCC	GCGCGCGGCT	CGGGGTTCGG	7140
GGTTCGTCCG	CCCCGGCCGG	GTGGAAGGTC	CCGTGCCCCG	CGTCTGCTGC	GTCGCGCGTC	7200
GTGCGCGGTG	GGGGCGGTGT	GCGTGCGGTG	TGGTGGTGGG	GGAGGAGGAA	GGCGGGTCCG	7260
GAAGGGGAAG	GGTGCCGGCG	GGGAGAGAGG	GTGCGGGGAG	CGCGTCCCGG	TCGCGCGGCT	7320

TCCGCGCGCG	CGCGCGCGCG	GCGCGCGCGG	GTCCGCGCGG	CCGCGCGCGT	CCGCGCGCGG	7380
TCCCTCCTCC	CGCGCGCGCG	CCTCCGAGGC	CCCGCGCGGT	CTCCTCGCGG	TCCCGCGCGG	7410
TACGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CTCGCGCGCG	GTCCGCGCGG	CGCGCGCGCG	7440
CGCGCGCGCG	CGCGCGCGCG	GCGCGCGCGG	CGCGCGCGCG	GTGTCGCGCG	CGCGCGCGCG	7460
CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	7480
CGCGCGCGCG	CGCGCGCGCG	GAGCTTCCCG	GTCCGCGCGG	CGCGCGCGCG	CGCGCGCGCG	7500
CTCGGACCGG	TCCCGCGCGG	CTCCGCGCGG	GAGACGCGCG	GGGCGGTCCG	CGCGCGCGCG	7520
CGCGCGCGCG	CGCGCGCGCG	CCCTCCGGTC	GTCCCGCGCG	GGCGCGCGCG	CGCGCGCGCG	7540
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GGAGCGTCCG	GCGCGCGCGG	GGCGCGCGCG	GATTCCCGCG	GTCCGTCGCG	CGAGCGCGCG	7580
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CGGGTCGGGG	CGGCGGCGGC	GGCGGGCGGT	GCGGCGGGCG	CGGGGGCGGC	GGGACCGAAA	8820
CCCCCCCCGA	GTGTTACAGC	CCCCCGGGCA	CGAGCACTCG	CCGAATCCCG	GGGCCGAGGG	8880
AGCGAGACCC	GTCGCGCGCG	TCTCCCCCTC	CCCGGCGCCC	ACCCCGCGCG	GGAATCCCCC	8940
GCGAGGGGGG	TCTCCCCCGC	GGGGGGCGCG	CGGCGTCTCC	TCGTGGGGGG	GCCGGGCCAC	9000
CCCTCCACAG	GCGCGACCGC	TCTCCACCCG	CTCTCCCCCG	CGCCCCCGCC	CCGGCGACGG	9060
GGGGGGTGCC	GCGCGCGGGT	CGGGGGGGCG	CGGGGACTGT	CCCCAGTGCG	CCCCGGGCGG	9120
GTGCGCGCGT	CGGGCCCCGG	GGAGGTTCTC	TCGGGGCCAC	GCGCGGTGCC	CCCGAAGAGG	9180
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TGAAACACGG	ACCAAGGAGT	CTAACACGTG	CGCGAGTCGG	GGGCTCGCAC	GAAAGCCGCC	9300
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TCCAGTCCGC	CGAGGGCGCA	CCACCGGCCC	GTCTCGCCCC	CCGCGCCGGG	GAGGTGGAGC	9420
ACGAGCGCAC	GTGTTAGGAC	CCGAAAGATG	GTGAACTATG	CCTGGGCAGG	GCGAAGCCAG	9480
AGGAACTCT	GGTGGAGGTC	CGTAGCGGTC	CTGACGTGCA	AATCGGTGCT	CCGACCTGGG	9540
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CGAATGATTA	GAGGTCTTGG	GGCCGAAACG	ATCTCAACCT	ATTCTCAAAC	TTTAAATGGG	9720
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TTTTGGTAAG	CAGAACTGGC	GCTGCGGGAT	GAACCGAACG	CCGGGTTAAG	GCGCCCCGATG	9840
CCGACGCTCA	TCAGACCCCA	GAAAAGGTGT	TGGTTGATAT	AGACAGCAGG	ACGGTGGCCA	9900
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CGGCGGCGGC	GGCGGGGGTG	TGGGGTCTTT	CCCCCGCCCC	CCCCCGCACG	CCTCCTCCCC	10140
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CAGGTGCAGA	TCTTGGTGGT	AGTAGCAAAT	ATTCAAACGA	GAACCTTGAAG	GGCCGAAGTG	10320
GAGAAGGGTT	CCATGTGAAC	AGCAGTTGAA	CATGGGTGAG	TCGGTCTCTGA	GAGATGGGCG	10380
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CGCCCGCGGT	GGACGAGGCG	GCGCCCCCCC	CCACGCCCCG	GGCACCCCCC	TCGCGGCCCT	10920
CCCCCGCCCC	ACCCGCGCGC	GCCGCTCGCT	CCCTCCCCAC	CCCGCGCCCT	CTCTCTCTCT	10980
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GTGAGACCG	CTGACTCCCT	CTACCTTGGG	TTCCCTCGGC	CCCACCCTGG	AACGCCGGGC	36000
CTTGGCAGAT	TCTGGCCCTT	TCTGGCCCTT	CAGTCGCTGT	CAGAAACCCC	ATCTCATGCT	36060
CGGATGCCCC	GAGTGACTGT	GGCTCGCACC	TCTCCGGAAA	CATTGGAAAT	CTCTCCTCTA	36120
CGCGCGGCCA	CCTGAAACCA	CAGGAGCTCG	GGACACACGT	GCTTTCGGGA	GAGAATGCTG	36180
AGAGTCTCTC	CCCGACTCTC	TCTTGACTTG	AGTCTTCTGT	GGGTGCGTGG	TTAAGACGTA	36240
GTGAGACCCAG	ATGTATTAAC	TCAGGCCGGG	TGCTGGTGGC	TCACGCCTGT	AACCCCAACA	36300
CTTTGGGAGG	CCGAGGCCGT	AGGATCCCTC	GAGGAATCGC	CTAACCCCTG	GGAGGTTGAG	36360
GTTGCAGTGA	GTGAGCCATA	GTGTGTGCAC	TGTGCTCCAG	TCTGGGCGAA	AGACAGAATG	36420
AGGCCCTGCC	ACAGGCAGGC	AGGCAGGCAG	GCAGGCAGAA	AGACAACAGC	TGTATTATGT	36480
TCTTCTCAGG	GTAGGAAGCA	AAAATAACAG	AATACAGCAC	TTAATTAATT	TTTTTTTTTT	36540
CCTTCGGACG	GATTTTCACT	CTTGGTGGCC	ACGCTGGAGT	GCAGTGGCAC	CATCTTGGCT	36600
CACCGCAACC	TCCACCTCCC	GCGTTCAAGC	GATTCTCCTG	CCTCAGCCTC	CTGAGTAGCT	36660
GGGATTACAG	GGAGGAGCCA	CCACACCCAG	CTGATTTTGT	ATTGTTAGTA	GAGACGGCAT	36720
TTCTCCATGT	GGGTCTAGGCT	GGTCTCGAAC	TGGCGACCCC	AGTGGATCTG	CCCCCCCCCG	36780
CCTCCCAAAG	TGCTGGGGTG	ACAGGCGTGA	GCCATCGTGA	CTGGCCGGCT	ACGTTTATTT	36840
ATTTATTTTT	TTAATTATTT	TACTTTTTTT	TAGTTTTCCA	TTTTAATCTA	TTTATTTATT	36900
TACATTTATT	TATTTATTTA	TTTATTTACT	TATTTATTTA	TTTTCGAGAC	AGACTCTCGC	36960
TCTGCTGCCC	AGGCTGGAGT	GCAGCGGCGT	GATCTCGGCT	CACTGCAACG	TCCGCCTCCC	37020
GGGTTCACGC	CATTCTCCTG	CCTCAGCCTC	CCAAGTAGCT	GGGACTACAG	GCGCCCGCCA	37080
CCGTGCCCCG	CTAACTTTTT	GTATTTTGAG	TAGAGTAGGG	GTTTCACTGT	GGTAGCCAGG	37140
ATGGTCTCGA	TCTCCTGACC	CCGTGATCCG	TCCACCTCGG	CCTCCCAAAG	TGCTGGGATG	37200
ACAGGCGTGA	GCCACCGGCC	CCGGCCTATT	TATCTATTTA	TTAACTTTGA	GTCCAGGTTA	37260
TGAAACCAAG	TAGTTTTTGT	AATTTTTTTT	TTTTTTTTTT	TTTTTTGAGA	CGAGGTTTCA	37320
CCGTGTTGCC	AAGGCTTGGA	CCGAGGGATC	CACCGGCCCT	CGGCCTCCCA	AAAGTCCGGG	37380
GATGACAGGC	GCGAGCCTAC	CGCGCCCGGA	CCCCCCTTT	CCCCTTCCCC	CGCTTGCTTT	37440
CCCGACAGAC	AGTTTACAGG	CAGAGCGTTT	GGCTGGCGTG	CTTAAACTCA	TTCTAAATAG	37500
AAATTTGGGA	CGTCAGCTTC	TGGCCTCACG	GACTCTGAGC	CGAGGAGTCC	CCTGGTCTGT	37560
CTATCACAGG	ACCGTACACG	TAAGGAGGAG	AAAAATCGTA	ACGTTCAAAG	TCAGTCATTT	37620
TGTGATACAG	AAATACACGG	ATTCACCCAA	AAACACAGAA	CCAGTCTTTT	AGAAATGGCC	37680
TTAGCCCTGG	TGTCCGTGCC	AGTGATTCTT	TTGCGTTTGG	ACCTTGACTG	AGAGGATTCC	37740
CAGTCGGTCT	CTCGTCTCTG	GACGGAAGTT	CCAGATGATC	CGATGGGTGG	GGGACTTAGG	37800
CTGCGTCCCC	CCAGGAGCCC	TGGTCGATTA	GTTGTGGGGA	TCGCCTTGGA	GGGCGCGGTG	37860
ACCCACTGTG	CTGTGGGAGC	CTCCATCCTT	CCCCCACCC	CCTCCCCAGG	GGGATCCCAA	37920
TTTATTTCCG	GCTGACACGC	TCACTGGCAG	GCGTCGGGCA	TCACCTAGCG	GTCATGTTA	37980
CTCTGAAAAC	GGAGGCCTCA	CAGAGGAAGG	GAGCACCAGG	CCGCCTGCGC	ACAGCCTGGG	38040
GCAACTGTGT	CTTCTCCACC	GCCCCGCCCC	CCACCTCCAA	GTTCTCCTCT	CCCTTGTTGC	38100
CTAGGAAATC	GCCACTTTGA	CGACCGGGTC	TGATTGACCT	TTGATCAGGC	AAAAACGAAC	38160
AAACAGATAA	ATAAATAAAA	TAACACAAAA	GTAACAACT	AAATAAAATA	AGTCAATACA	38220
ACCCATTACA	ATACATAAAG	ATACGATACG	ATAGGATGCG	ATAGGATACG	ATAGGATACA	38280
ATACAATAGG	ATACGATACA	ATACAATACA	ATACAATACA	ATACAATACA	ATACAATACA	38340
ATACAATACA	ATACAATACG	CCGGGCGCGG	TGGCTCATGC	CTGTCATCCC	GTCACCTTGG	38400
GATGCCGAGG	TGGACGCATC	ACCTGAAGTC	GGGAGTTGGA	GACAAGCCCC	ACCAACATGG	38460
AGAAATCCCC	TCTCAATTGA	AAATACAAAA	CTAGCCGGGC	GCGGTGGCAC	ATGCCTATAA	38520

TCCAGCTGC	TAGGAAGGCT	GAGGCAGGAG	AATCGCTTGA	ACCTGGGAAG	CGGAGGTTGC	38580
AGTAGGCGGA	GATTGCGCCA	TCCGACTCCA	GTCTGAGCAA	CAAGAGCGAA	ACTCGGTCTC	38640
AAAAATAAA	ACATAAATAA	ATACATAACAT	ACATACATAC	ATACATAACAT	ACATACATAC	38700
ATAAAATTAAA	ATAAAATAAA	AAAAATAAA	AAATAAAATGG	GCCCTGCGCG	GTGCTCAAG	38760
CCTGTCATCC	CCTCACTTTG	GGAGGCCAAG	GCCGCTGGAT	CAAGAGGCGG	TCAGACCAAC	38820
AGGGCCAGTA	TGGTGAACCC	CCGTCTCTAC	TCACAATACA	CAACATTAGC	CGGGCGCTGT	38880
GCTGTGCTGT	ACTGTCTGTA	ATCCCAGCTA	CTCGGGAGGC	CGAGCTGAGG	CAGGAGAATC	38940
GCTTGAACCT	GGGAGGCGGA	GTTTGCAGTG	AGCCGAGATC	GCGCCACTGC	AACCCAGCCT	39000
GGGCGACAGA	GCGAGACTCC	GTCTCCAAAA	AATGAAAATG	AAAATGAAAC	GCAACAAAAAT	39060
AATTAATAAAG	TGAGTTTCTG	GGGAAAAAGA	AGAAAAGAAA	AAAGAAAAAA	ACAACAAAAAC	39120
AGAACAACCC	CACCGTGACA	TACACGTACG	CTTCTCGCCT	TTCGAGGCCT	CAAAACACGTT	39180
AGGAATTATG	CGTGATTTCT	TTTTTTAACT	TCATTTTATG	TTATTATCAT	GATTGATGTT	39240
TCGAGACGGA	GTCTCGGAGG	CCCGCCCTCC	CTGGTTGCCC	AGACAACCCC	GGGAGACAGA	39300
CCCTGGCTGG	GCCCCGATTGT	TCTTCTCCTT	GGTCAGGGGT	TTCCTTGTCT	TTCTTCGTGT	39360
CTTTAACCCG	CGTGGACTCT	TCCGCTTCGG	GTTTGACAGA	TGGCAGCTCC	ACTTTAGGCC	39420
TTGTTGTTGT	TGGGGACTTT	CCTGATTCTC	CCCAGATGTA	GTGAAAGCAG	GTAGATTGCC	39480
TTGCCCTGGCC	TTGCCCTGGCC	TTGCCCTTTT	TTTTCTTTCT	TCTTTCTTTA	TTACTTTCTC	39540
TTTCTTTCTT	TCTTCTTTCT	CTTTTTTTTG	AGACAGAGTT	TCACTCTTGT	TGCCAGGCCT	39600
AGAGGGCAAT	GGCGCATCT	CGGCTCACCG	CACCCCTCCGC	CTCCAGGTT	CAAGCGATTC	39660
TCCTGCCTCA	GCCTCCTGAT	TAGCTGGGAT	TACAGGCATG	GGCCACCGTG	CTGGCTGATG	39720
TTTGTACTTT	TAGTAGAGAC	GGTGTTTTTT	CATGTTGGTC	AGGCTGGTCT	CCCACTCCCA	39780
ACCTCAGGTG	CTCCGCTGCG	CTTAGCCTCG	CAAAGTGCTG	GGATGACAGG	CGTGCAACCG	39840
CGCCAGCCT	CTCTCTCTCT	CTCTCTCTCT	CTCGCTCGCT	TGCTTGCTTG	CTTTCTGCTT	39900
TTCTTGCTTT	CCCGTTTTCT	TGCTTTCTTT	CTTTCTTTCT	TTTCTTTCAT	GCTTGCTTTT	39960
TTGCTTGCTT	GCTTGCTTTT	GTGCTTTCTT	GCTTTCTCTG	TTTCTTTCTT	TCTTTCTTTT	40020
TTTCTTTCTT	TTGTTTCTTT	CTTGCTTGCT	TTCTTGCTTG	CTTGCTTGCT	TTCTTGCTTT	40080
CTTGCTTTCT	TGTTTTCTTT	CTTTCTTTCT	TTCTTTCTTT	TTCTTTCTTT	TTCTTTCTTT	40140
GCTTGCTTGC	TTTCGTGCTT	TCTTGTTTTT	TCGATTTCTT	TCTTTCTTTT	GTTTCTTTCT	40200
TGCTTGCTTT	CTTGCTTGCT	TGCTTTCTGT	CTTCTTGCTT	TCCTGTTTTT	TTTCTTTCTT	40260
TCTTTCTTTT	GTTTCTTTCT	TGCTTGCTTT	CTTGCTTGCT	TGCTTTCTGT	CTGCTTGCTT	40320
TCTCGATTTT	TTTCTTTCTT	TTGTTTCTTT	CCTGCTTGCT	TTCTTGCTTG	ATTGCTTTCT	40380
TGCTTTCTTG	CTTTCTTGTT	TTCTTTCTTT	CTTTTGTTTT	TTTCTTTCTT	GCTTTCTTGT	40440
TTTCTTGCTT	TCTTGCTTGC	TTGCTTTCTG	GCTTTCTTGT	TTTCTTGCTT	TCTTTCTTTT	40500
GTTTCTTTCT	TGCTTGCTTT	CTTGCTTTCT	TGTTTTCTTG	CTTTCTTGCT	TGCTTGCTTT	40560
CGTGCTTTCT	TTCTTGCTTT	CTTTTCTTTT	TTTCTTTTCT	TTTCTTTTCT	TTCTTGCTTT	40620
CTTTTCTTTT	ATCATCATCT	TTCTTTCTTT	CCTTTCTTTT	TTTCTTTCTT	TCTATCTTTT	40680
TTTCTTTCTT	CTTTTCTTTT	TTCTTTCTTT	TCTTTCTGTT	TCGTCTTTT	GAGACGAGT	40740
TTCACCTCTG	TTTCCACGGC	TAGAGTGCAA	TGGCGCGATC	TTGGCTCACC	GCACCTTCCG	40800
CCTCCCGGGT	TCGAGCGCTT	CTCCTGCCTC	CAGCCTCCCG	ATTAGCGGGG	ATTGACAGGG	40860
AGGCACCCCC	ACGCCTGGCT	TGGCTGATGT	TTGTGTTTTT	AGTAGGCACG	CCGTGCTCTC	40920
CCATGTTGCT	CAGGCTGGTC	TCCAACCTCC	GACCTCCTGT	GATGCGCCCA	CCTCGGCTCT	40980
TCGAAGTGCT	GGGATGACGG	GGGATGACGAC	CGTGCCCGGC	CTGTTGACTC	ATTTGCTTTT	41040
TTTATTTCTT	TCGTTTCCAC	GCGTTTACTT	ATATGTATTA	ATGTAAACGT	TTCTGTACGC	41100
TTATATGCAA	ACAACGACAA	CGTGTATCTC	TGCATTGAAT	ACTCTTGCGT	ATGGTAAATA	41160
CGTATCGGTT	GTATGGAAAT	AGACTTCTGT	ATGATAGATG	TAGGTGTCTG	TGTTATACAA	41220
ATAAATACAC	ATCGCTCTAT	AAAGAAGGGA	TCGTGAGATA	AGACGTTTAT	TTTACGTATG	41280
AAAAGCGTCG	TATTTATGTG	TGTAAATGAA	CCGAGCGTAC	GTAGTTATCT	CTGTTTTCTT	41340
TCTTCTCTCT	CTTCGTGTTT	TTCTTCTTCT	CTTTCTTCTT	TTCTTCTTCT	CTTTAGGTTT	41400
TTCTTCTCTT	CTTCTTTTCC	TTCTTTCTCT	CTTTCTGTCC	TTTTTTCTCT	CGTGCTTTAT	41460
TTCTTCTTCT	TTCCCTGTGT	TTCTTTCTTT	TTTCTTTCTT	CTCTGTTTCT	TTTTCCCTTC	41520
TTTCTTCTGT	TTCTTTCTCT	ATTCTTTCTT	TCTTTTCTGT	TGTTTCTTTT	CTTCCCGTCT	41580
GTCTTTTAAA	AAATTGGAGT	GTTTCAGAAG	TTTACTTTGT	GTATCTACGT	TTTCTAAATT	41640
GTCTCTCTTT	TCTCCATTTT	CTTCTCTCCT	CCCTCCCTCC	CTCCCTGCTC	CCTTCCCTCC	41700
CTCCTTCCCT	TTCCGCATCT	GTCTCTTTT	CCCACTCCCC	TCCCCCCTGC	TGTCTCTGCG	41760
TGGATTCCGG	AAGAGCCTAC	CGATTCTGCC	TCTCCCTGTG	TCTGCAGCGA	CCCCGCGACC	41820
GAGTCCTTGT	TGTTTCTTTT	TCCCTCCCTC	CCTCCCTCCC	TCCCTCCCTC	CCTCCCTGCT	41880
TCCGAGAGGC	ATCTCCAGAG	ACCGCGCCGT	GGGTTGTCTT	CTGACTCTGT	CGCGGTCGAG	41940
GCAGAGACGC	GTTTTGGGCA	CCGTTTGTGT	GGGGTTGGGG	CAGAGGGGCT	GCGTTTTTCGG	42000
CCTCGGGAAG	AGCTTCTCGA	CTCACGGTTT	CGCTTTTCGG	GTCCACGGGC	CGCCCTGCCA	42060
GCCGGATCTG	TCTCGCTGAC	GTCCGCGGCG	GTTGTGCGGC	TCCATCTGGC	GGCCGCTTTG	42120
AGATCGTGCT	CTCGGCTTCC	GGAGCTGCGG	TGGCAGCTGC	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	AGGCAGAGCT	CCGGAAGGCC	CGCGGTCGTC	AGCCCGGCTG	GCCCGGTGGC	42240
GCCAGAGCTG	TGGCCGGTCG	CTTGTGAGTC	ACAGCTCTGG	CGTGAGGTTT	TATGTGGGGG	42300
AGAGGCTGTC	GCTGCGCTTC	TGGGCCCCGG	GCGGGCGTGG	GGCTGCCCCG	GCCCGTCCGAC	42360
CAGCGCGCCG	TAGCTCCCGA	GGCCCGAGCC	GCGACCCGGC	GGACCCGGCG	GCGGTGGCGG	42420

AGGCTGGGGA	CGTCTTCCG	GGCCCGGTG	CGGTCCGCTC	ATCCTGGGCG	TCTGAGGCGG	42480
CGGCCGAATT	CGTTTCCGAG	ATCCCCGTGG	GGAGCCGGGG	ACCGTCCCGG	CCCCGTCCCG	42540
CGGCTGCCCC	GGAGCGGTCC	CCGGCCCGGG	CCGCGGTCCC	TCTGCGCGGA	TCTTTTCTGG	42600
CGAGTCCCCG	TGSCCAGTCG	GAGAGCGCTC	CCTGAGCCGG	TGCGGCCCCG	GAGGTCCGCG	42660
TGGCCCGGCT	TGGTCCCTTC	GTGTGTCCCG	GTGCTAGGAG	GGGCCCCGCG	AAAATGCTTC	42720
CGGTCCCCGC	TCTGGAGACA	CGGGCCGGCC	CCTGCGTGTG	GCCAGGGCGG	CCGGGAGGGC	42780
TCCCCGGCCC	GGCGTGTCC	CCGCGTGTGT	CCTTGGGTTG	ACCAAGAGGA	CCCCGGCGCG	42840
TCCGTGTGTG	GCTGCGATGG	TGGCGTTTTT	GGGGACAGGT	GTCCGTGTCC	GTGTCCGCGG	42900
TCGCCTGGGC	CGGCGGCGTG	GTGCGTGACG	CGACCTCCCG	GCCCCCGGGG	AGGTATATCT	42960
TTCGCTCCGA	GTGCGCAATT	TGGGCCGCGC	GGGTTATAT			42999

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCGCGCG	GCCCCCGTGT	TCGCCGTTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCAGT	GCCGTTGTGG	AGTGCCTCGC	TCTCCTCCTC	CTCCCCGSCA	120
GCGTTCCAC	GGTTGGGGAC	CACCGGTGAC	CTCGCCCTCT	TGGGGCCTGG	ATCCG	175

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGGAAC	GGCGGGGTCTG	60
GTCGTGCCCC	GCGCCGGACG	TGTGTGCGGG	CCCACTTCCC	GCTCGAGGGT	GGCGGTGGCG	120
GCGGCGTTGG	TAGTCTCCCC	TGTTGCGTCT	TCCCGGGCTC	TTGGGGGGGG	TGCCGTCTGT	180
TTCGGGGCCG	GCGTTGCTTG	GCTTACGCAG	GCTTGGTTTG	GGACTGCCTC	AGGAGTCGTG	240
GGCGGTGTGA	TTCCCGCCCG	TTTTGCCTCG	CGTCTGCCTG	CTTTGCCTCG	GGTTTGCTTG	300
GTTCTGTCT	CGGGAGCGGT	GGTTTTTTTT	TTTTTCGGGT	CCCGGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCGTCCGC	CCCTGCCGCC	GGTGGGTTTT	CGTTTCGGGC	TGTGTTCTGT	420
TCCCTTTCCC	CGTTTCGCCG	TCGGTTCTCC	CCGGTCGGTC	GGCCCTCTCC	CCGGTCGGTC	480
GCCCGGCCGT	GCTGCCGGAC	CCCCCTTCT	GGGGGGGATG	CCCGGGCAGC	CACGCGTCCG	540
GGCGGCCACT	GTGGTCCGGG	AGCTGCTCGG	CAGGCGGGTG	AGCCAGTTGG	AGGGGCGTCA	600
TGCCCCCGCG	GGCTCCCGTG	GCCGACGCGG	CGTGTTCTTT	GGGGGGGCCT	GTGCGTGCGG	660
GAAGGCTGCG	CACGTTGTCT	GTCCTTGCGA	GGGAAAGAGG	CTTTTTTTTT	TTAGGGGGTG	720
GTCCTTCGTC	GTCCGTCGCG	CGGTGATCC	GGCCT			755

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAGGTG	CGTCTGCGGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCTCCG	GGAAGGCGTT	60
TAGCGGGTAC	CGTCGCCCGC	CCGAGGTGGG	CGCACGTCGG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGGCGGG	GGCTCCGGTC	GATGTCTTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAGCC	TCCGCCTGTG	GGCTTCGTCG	GCCGTCTCCC	CCCCCTCAC	GTCCCTCGCG	240
AGCGAGCCCG	TCCGTTGAC	CTTCCTTCCG	CCTTCCCCC	ATCTTTCCGC	GCTCCGTTGG	300
CCCCGGGGTT	TTCACGGCGC	CCCCACGCT	CCTCCGCCTC	TCCGCCCCGTG	GTTTGACGC	360
CTGGTTCGG	TCTCCCCGCC	AAACCCCGGT	TGGGTTGGTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGGTCTCCC	AACCCCGGC	CGGAAGGGTT	CGGGGGTTCC	GGG		463

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCTT	TTCCGGCTCC	GGCCGGGGGG	60
GGCGGCCCCG	GGCGGTTTGG	TGAGTTAGAT	AACCTCGGGC	CGATCGCACG	CCCCCGTGG	120
CGGCGACGAC	CCATTGGAAC	GTCTGCCCTA	TCAACTTTCG	ATG3TAGTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTTCGATTCC	GGAGAGGGAG	CCTGAGAAAC	240
GGCTACCACA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAT	ACAGGACTCT	TTCGAGGCCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAAGCAG					378

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGG3AGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTCACCGC	CCGTCCCCGC	CCCTTGCCCTC	TCG3CGCCCC	CTCGATGCTC	180

TTAGCTGAST	TGTCCCGCGG	GGCCCCGAAG	GTTTACTTTG	AAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCC	GAGCCGCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGGCTT	300
CCTATTTTGT	TTGGTTTTCG	GAAGTGAGCC	CATGATTAA	GGAAACGGCC	GGGGGATTTC	360
CCTTATTGCG	CCCCCCTA					378

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCTTTTC	CGCTCCCCGT	TCCTCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCTTCTTT	60
TCCCCTCTCC	GGAGGGGGGG	GAGGTGGGGG	CGCGTGGGCG	GGGTCCGGGG	TGGGGTGGGC	120
GGGGGACCGC	CCCCGGCCGG	CAAAAGGCCG	CCGCCGGGCG	CACTTCAACC	GTAGCGGTGC	180
GCCGCGACCG	GCTACGAGAC	GGCTGGGAAG	GCCCCGACGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGCGCC	GAACCACTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCGGGGCC	GAGGGGAAGC	CCGATACCCG	TCGCCGCGCT	TTTCCCCTCC	360
CCCCGTCCGC	CTCCCGGGCG	GGCGTGGGGG	TGGGGGCCCG	GCCGCCCTC	CCACGCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGGC	480
GGACTGTCTC	CAGTGCGCC	CGGCGTCTG	CGCGCCGTCG	GGCCCGGGGG	GTCTCTCTCG	540
TCACGCCGCC	CCCGACGAAG	CCGAGCGCAC	GGGTCGGGCG	GCGATGTCGG	CTACCCACCC	600
GACCCGTCTT	GAAACACGGA	CCAAGGAGTC	TAACGCGTGC	GCGAGTCAGG	GGCTCGCAGC	660
AAAGCCGCCG	TGCGCAATG	AAGGTGAAGC	GCCCCGTCCG	GGGGCCCGAG		720

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTISENSE: NO

## (v) FRAGMENT TYPE:

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT	CCAGTCCGCC	GAGGGCGCAC	CACCGGCCCG	TCTCGCCCGC	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAAGTATGC	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTCGTC	180
CGACCTGGGT	ATAGGGGCGA	AAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTTATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCCGGA	AACGATCTCA	AACTATTCT	CAAACTTTAA	360
ATGGGTAAAG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGCG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTTT	GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTTAAGGCGC	480
CCGATGCCGA	CGCTCATCAG	ACCCAGAAAA	AGGTGTTGGT	TGATATAGAC	AGCAGGACGG	540
TGGCCATGGA	AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTCGC	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	GCCGC				685

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG

33

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTAC AGAAGAGAGG TGGCTCGGCC TGC

33

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCCT AACCCCTAACC CTAACCCTAA  
CCCTAACCCT AACCCGGGAT

60

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21